

SEQUENCE LISTING

<110> SUN Y LIMITED

<120> coding for a protein having glycosyl transferase  
aurone

<220>  
<223> Nucleotide sequence coding for a protein having  
glycosyl transferase to aurone

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Met Gly Lys Leu His Ile Ala Leu Phe Pro Val Met  
1 5 10  
gct cat ggt cac atg atc cca atg ttg gac atg gcc aag ctc ttt acc 159  
Ala His Gly His Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr  
15 20 25  
tca aga ggc ata caa aca aca atc att tgg act ctc gcc ttc gct gat 207  
Ser Arg Gly Ile Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp  
30 35 40  
ccg ata aac aaa gct cgt gat tgg ggc ctc gat att gga cta agc atc 255  
Pro Ile Asn Lys Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile  
45 50 55 60  
ctc aaa ttc cca cca gaa gga tca gga ata cca gat cac atg gtg agc 303  
Leu Lys Phe Pro Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser  
65 70 75

ctt gat cta gtt act gaa gat tgg ctc cca aag ttt gtt gag tca tta 351  
 Leu Asp Leu Val Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu  
 80 85 90  
 gtc tta tta caa gag cca gtt gag aag ctt atc gaa gaa cta aag ctc 399  
 Val Leu Leu Gln Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu  
 95 100 105  
 gac tgt ctc gtt tcc gac atg ttc ttg cct tgg aca gtc gat tgt gcg 447  
 Asp Cys Leu Val Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala  
 110 115 120  
 gct aag ttc ggt att ccg agg ttg gtt ttc cac gga acg agc aac ttt 495  
 Ala Lys Phe Gly Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe  
 125 130 135 140  
 gcg ttg tgt gct tcg gag caa atg aag ctt cac aag cct tat aag aat 543  
 Ala Leu Cys Ala Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn  
 145 150 155  
 gta act tct gat act gag aca ttt gtt ata ccg gat ttc ccg cat gag 591  
 Val Thr Ser Asp Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu  
 160 165 170  
 ctg aag ttt gtg agg act caa gtg gct ccg ttt cag ctt gcg gaa acg 639  
 Leu Lys Phe Val Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr  
 175 180 185  
 gag aat gga ttc tca aag ttg atg aaa cag atg acg gag tct gtt ggt 687  
 Glu Asn Gly Phe Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly  
 190 195 200  
 aga agc tac ggt gtt gtg gtt aac agt ttt tat gag ctc gag tcg act 735  
 Arg Ser Tyr Gly Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr  
 205 210 215 220  
 tat gtg gat tat tac aga gag gtt ttg ggt aga aag tct tgg aat ata 783  
 Tyr Val Asp Tyr Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile  
 225 230 235  
 ggg cct ctg ttg tta tcc aac aat ggc aat gag gaa aaa gta caa agg 831  
 Gly Pro Leu Leu Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg  
 240 245 250  
 gga aag gaa tct gcg att ggc gaa cac gaa tgc ttg gct tgg ttg aat 879  
 Gly Lys Glu Ser Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn  
 255 260 265

tcc aag aag cag aat tcg gtt gtt tac gtt tgt ttt gga agt atg gcg 927  
 Ser Lys Lys Gln Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala  
 270 275 280  
 act ttt act cca gcg cag ttg cgc gaa act gcg att gga ctc gag gaa 975  
 Thr Phe Thr Pro Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu  
 285 290 295 300  
 tca ggc caa gag ttc att tgg gta gtt aaa aag gcc aaa aac gaa gaa 1023  
 Ser Gly Gln Glu Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu  
 305 310 315  
 gaa gga aaa gga aaa gaa gaa tgg ctg cca gaa aat ttt gag gaa aga 1071  
 Glu Gly Lys Gly Lys Glu Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg  
 320 325 330  
 gtg aaa gat aga ggc ttg atc ata aga gga tgg gcg ccg caa ttg ttg 1119  
 Val Lys Asp Arg Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu  
 335 340 345  
 ata ctc gat cat cct gcg gta gga gct ttc gtg acg cat tgt gga tgg 1167  
 Ile Leu Asp His Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp  
 350 355 360  
 aat tcg acg ttg gaa gga ata tgc gcc ggt gtg cct atg gtg act tgg 1215  
 Asn Ser Thr Leu Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp  
 365 370 375 380  
 cca gtt ttc gca gag cag ttt ttc aat gag aag ttt gtg aca gag gtt 1263  
 Pro Val Phe Ala Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val  
 385 390 395  
 ttg ggg acc ggt gtt tcg gtt ggg aat aag aag tgg cta agg gca gca 1311  
 Leu Gly Thr Gly Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala  
 400 405 410  
 agt gaa ggt gtg tcg agg gag gca gtg acg aac gcg gtg cag cgt gtt 1359  
 Ser Glu Gly Val Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val  
 415 420 425  
 atg gtg gga gaa aat gcg tcg gag atg aga aag cga gcg aag tat tat 1407  
 Met Val Gly Glu Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr  
 430 435 440  
 aag gaa atg gcg agg cgg gcg gtt gag gaa ggc ggt tcg tct tat aat 1455  
 Lys Glu Met Ala Arg Arg Ala Val Glu Glu Gly Gly Ser Ser Tyr Asn  
 445 450 455 460

ggt ttg aat gag atg ata gag gat ttg agt gtg tac cgt gct cca gaa 1503  
 Gly Leu Asn Glu Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu  
 465 470 475  
 aaa caa gac tta aac tagattctta tagatgactt ctagtgtgac aattgtaatt 1558  
 Lys Gln Asp Leu Asn  
 480  
 ttttgccttt tattcaagtt tcctcattag tgttgagagc tttccctgta ttttcagaat 1618  
 tggtttgttc aatttttaca tgatttgtga tagatagctg catagtttct agctgttaac 1678  
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 aaaaaaaaaa aaa 1751

<210> 2

<211> 481

<212> PRT

<213> Antirrhinum majus

<220>

<223> Amino acid sequence of a protein having glycosyl transferase to aurone

<400> 2

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 Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr Ser Arg Gly Ile  
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 Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp Pro Ile Asn Lys  
 35 40 45  
 Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile Leu Lys Phe Pro  
 50 55 60  
 Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser Leu Asp Leu Val  
 65 70 75 80  
 Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu Val Leu Leu Gln  
 85 90 95  
 Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu Asp Cys Leu Val  
 100 105 110  
 Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala Ala Lys Phe Gly  
 115 120 125

Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe Ala Leu Cys Ala  
 130 135 140  
 Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn Val Thr Ser Asp  
 145 150 155 160  
 Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu Leu Lys Phe Val  
 165 170 175  
 Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr Glu Asn Gly Phe  
 180 185 190  
 Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly Arg Ser Tyr Gly  
 195 200 205  
 Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr Tyr Val Asp Tyr  
 210 215 220  
 Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile Gly Pro Leu Leu  
 225 230 235 240  
 Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg Gly Lys Glu Ser  
 245 250 255  
 Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn Ser Lys Lys Gln  
 260 265 270  
 Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala Thr Phe Thr Pro  
 275 280 285  
 Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu Ser Gly Gln Glu  
 290 295 300  
 Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu Glu Gly Lys Gly  
 305 310 315 320  
 Lys Glu Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg Val Lys Asp Arg  
 325 330 335  
 Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu Ile Leu Asp His  
 340 345 350  
 Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu  
 355 360 365  
 Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala  
 370 375 380  
 Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val Leu Gly Thr Gly  
 385 390 395 400  
 Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala Ser Glu Gly Val  
 405 410 415  
 Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val Met Val Gly Glu  
 420 425 430

Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr Lys Glu Met Ala  
 435 440 445  
 Arg Arg Ala Val Glu Glu Gly Gly Ser Ser Tyr Asn Gly Leu Asn Glu  
 450 455 460  
 Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu Lys Gln Asp Leu  
 465 470 475 480  
 Asn

<210> 3  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400>  
 ataactacat atgggacaac tccac

25

<210> 4  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 4  
 cagaacagga tccacacgta attta

25

<210> 5  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 5

ataactacat atgggaaaac ttcac

25

<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 6

gaacaggatc cacacactag aagtca

26

<210> 7

<211> 1750

<212> DNA

<213> Petunia hybrida

<220>

<223> Nucleotide sequence coding for a protein having  
glycosyl transferase to aurone

<400> 7

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53

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1

5

caa cca cat ttt gtg ctg ctt cct ttc atg gca caa ggc cat aca aat  
Gln Pro His Phe Val Leu Leu Pro Phe Met Ala Gln Gly His Thr Asn

101

10

15

20

ccc atg att gac atc gca cgc cta ttg gca caa cgc gga gtt ata atc  
Pro Met Ile Asp Ile Ala Arg Leu Leu Ala Gln Arg Gly Val Ile Ile

149

25

30

35

acc att ctt act aca cac ttt aat gcc act aga ttc aag aca gtc gtt  
Thr Ile Leu Thr Thr His Phe Asn Ala Thr Arg Phe Lys Thr Val Val

197

40

45

50

Handwritten notes on the left margin, including a large 'B' and some illegible text.

gat cgg gca gta gtg gca gca cta aag att cag gta gtt cac ctc tat 245  
Asp Arg Ala Val Val Ala Ala Leu Lys Ile Gln Val Val His Leu Tyr  
55 60 65 70  
ttt cca agc tta gag gct gga cta cct gaa ggg tgt gaa gct ttc gac 293  
Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu Gly Cys Glu Ala Phe Asp  
75 80 85  
atg ctt cct tca atg gat ttc gca atg aaa ttc ttt gat gct acc agt 341  
Met Leu Pro Ser Met Asp Phe Ala Met Lys Phe Phe Asp Ala Thr Ser  
90 95 100  
agg ctt caa cca caa gtg gaa gaa atg ctt cat gaa ctg caa ccg tca 389  
Arg Leu Gln Pro Gln Val Glu Glu Met Leu His Glu Leu Gln Pro Ser  
105 110 115  
cca agt tgc ata ata tot gat atg tgt ttt cca tgg aca act aat gtt 437  
Pro Ser Cys Ile Ile Ser Asp Met Cys Phe Pro Trp Thr Thr Asn Val  
120 125 130  
gca caa aaa ttc aac att cct agg ctt gtt ttt cat ggg atg tgc tgt 485  
Ala Gln Lys Phe Asn Ile Pro Arg Leu Val Phe His Gly Met Cys Cys  
135 140 145 150  
ttt tot tta ttg tgc ttg cac aat ttg aga gat tgg aag gag ttg gag 533  
Phe Ser Leu Leu Cys Leu His Asn Leu Arg Asp Trp Lys Glu Leu Glu  
155 160 165  
tct gat ata gaa tat ttt caa gtt cca gga tta cat gac aaa att gaa 581  
Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly Leu His Asp Lys Ile Glu  
170 175 180  
tta aac aaa gct cag ctt tca aat att gtt aag cca aga ggt cct gat 629  
Leu Asn Lys Ala Gln Leu Ser Asn Ile Val Lys Pro Arg Gly Pro Asp  
185 190 195  
tgg aat gaa ttt gca gat caa ctg aag aaa gca gaa gaa gaa gct tat 677  
Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys Ala Glu Glu Glu Ala Tyr  
200 205 210  
ggg ata gta gct aat agc ttt gaa gag tta gaa cca gaa tat gtc aag 725  
Gly Ile Val Ala Asn Ser Phe Glu Glu Leu Glu Pro Glu Tyr Val Lys  
215 220 225 230  
gga ttg gaa aag gca aaa ggc ttg aaa att tgg cca att ggt cct gtt 773  
Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile Trp Pro Ile Gly Pro Val  
235 240 245



tct ttg tgc aac aaa gag aaa cag gac aag gct gaa aga gga aac aag 821  
Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys Ala Glu Arg Gly Asn Lys  
250 255 260  
gct tca att gat gaa cac cag tgt cta aaa tgg cta gat tct tgg gga 869  
Ala Ser Ile Asp Glu His Gln Cys Leu Lys Trp Leu Asp Ser Trp Gly  
265 270 275  
gca aac tct gta ctc ttt gta tgt ctc ggg agc cta tcg cgc ctt cca 917  
Ala Asn Ser Val Leu Phe Val Cys Leu Gly Ser Leu Ser Arg Leu Pro  
280 285 290  
acg cca caa atg ata gag ctg gga ctt ggc tta gaa tcg tcg aaa aga 965  
Thr Pro Gln Met Ile Glu Leu Gly Leu Gly Leu Glu Ser Ser Lys Arg  
295 300 305 310  
ccc ttt att tgg gtt gtt aga cac aag tca gat gaa ttt aaa agt tgg 1013  
Pro Phe Ile Trp Val Val Arg His Lys Ser Asp Glu Phe Lys Ser Trp  
315 320 325  
cta gtt gaa gaa aat ttt gag gaa aga gtt aaa gga caa gga ctt tta 1061  
Leu Val Glu Glu Asn Phe Glu Glu Arg Val Lys Gly Gln Gly Leu Leu  
330 335 340  
atc cat ggt tgg gca cca caa gta cta ata tta tct cac act tca att 1109  
Ile His Gly Trp Ala Pro Gln Val Leu Ile Leu Ser His Thr Ser Ile  
345 350 355  
gga gga ttc ttg act cat tgt gga tgg aat tcg agt gtc gaa gga ata 1157  
Gly Gly Phe Leu Thr His Cys Gly Trp Asn Ser Ser Val Glu Gly Ile  
360 365 370  
tct gca ggc gtt cca atg atc act tgg cca atg ttt gct gaa caa ttc 1205  
Ser Ala Gly Val Pro Met Ile Thr Trp Pro Met Phe Ala Glu Gln Phe  
375 380 385 390  
tgt aat gaa agg cta ata gtg aat gta ctg aag aca gga gta aag gct 1253  
Cys Asn Glu Arg Leu Ile Val Asn Val Leu Lys Thr Gly Val Lys Ala  
395 400 405  
gga att gag aat cct gtt atg ttt gga gag gaa gaa aaa gtt gga gca 1301  
Gly Ile Glu Asn Pro Val Met Phe Gly Glu Glu Glu Lys Val Gly Ala  
410 415 420  
caa gtg agc aaa gat gat att aag atg gtt att gaa aga gtc atg ggc 1349  
Gln Val Ser Lys Asp Asp Ile Lys Met Val Ile Glu Arg Val Met Gly  
425 430 435

gaa gaa gag gaa gct gaa atg aga aga aaa aga gca aaa gag tta gga 1397  
 Glu Glu Glu Glu Ala Glu Met Arg Arg Lys Arg Ala Lys Glu Leu Gly  
 440 445 450  
 gaa aag gca aag agg gct atg gag gaa ggg ggt tcc tca cac ttc aac 1445  
 Glu Lys Ala Lys Arg Ala Met Glu Glu Gly Gly Ser Ser His Phe Asn  
 455 460 465 470  
 ttg aca cag ttg att caa gat gtc act gag caa gca aat att tta aaa 1493  
 Leu Thr Gln Leu Ile Gln Asp Val Thr Glu Gln Ala Asn Ile Leu Lys  
 475 480 485  
 tcc atc taggattata aagtcgattc caagttcctt ttacgatcaa tttctaacca 1549  
 Ser Ile  
 tctactagag atggttaacaa tccaaactgc gccttttttg cacaataatt attgttttat 1609  
 gttcagctag cacaaaaagt ttactattag tagaaatatt tcagctggaa ctgccgaact 1669  
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 tatcatatag gagctgattt t 1750

<210> 8

<211> 488

<212> PRT

<213> Petunia hybrida

<220>

<223> Amino acid sequence of a protein having glycosyl transferase to aurone

<400> 8

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 Ala Gln Gly His Thr Asn Pro Met Ile Asp Ile Ala Arg Leu Leu Ala  
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 Gln Arg Gly Val Ile Ile Thr Ile Leu Thr Thr His Phe Asn Ala Thr  
 35 40 45  
 Arg Phe Lys Thr Val Val Asp Arg Ala Val Val Ala Ala Leu Lys Ile  
 50 55 60  
 Gln Val Val His Leu Tyr Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu  
 65 70 75 80  
 Gly Cys Glu Ala Phe Asp Met Leu Pro Ser Met Asp Phe Ala Met Lys  
 85 90 95

Phe Phe Asp Ala Thr Ser Arg Leu Gln Pro Gln Val Glu Glu Met Leu  
 100 105 110  
 His Glu Leu Gln Pro Ser Pro Ser Cys Ile Ile Ser Asp Met Cys Phe  
 115 120 125  
 Pro Trp Thr Thr Asn Val Ala Gln Lys Phe Asn Ile Pro Arg Leu Val  
 130 135 140  
 Phe His Gly Met Cys Cys Phe Ser Leu Leu Cys Leu His Asn Leu Arg  
 145 150 155 160  
 Asp Trp Lys Glu Leu Glu Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly  
 165 170 175  
 Leu His Asp Lys Ile Glu Leu Asn Lys Ala Gln Leu Ser Asn Ile Val  
 180 185 190  
 Lys Pro Arg Gly Pro Asp Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys  
 195 200 205  
 Ala Glu Glu Glu Ala Tyr Gly Ile Val Ala Asn Ser Phe Glu Glu Leu  
 210 215 220  
 Glu Pro Glu Tyr Val Lys Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile  
 225 230 235 240  
 Trp Pro Ile Gly Pro Val Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys  
 245 250 255  
 Ala Glu Arg Gly Asn Lys Ala Ser Ile Asp Glu His Gln Cys Leu Lys  
 260 265 270  
 Trp Leu Asp Ser Trp Gly Ala Asn Ser Val Leu Phe Val Cys Leu Gly  
 275 280 285  
 Ser Leu Ser Arg Leu Pro Thr Pro Gln Met Ile Glu Leu Gly Leu Gly  
 290 295 300  
 Leu Glu Ser Ser Lys Arg Pro Phe Ile Trp Val Val Arg His Lys Ser  
 305 310 315 320  
 Asp Glu Phe Lys Ser Trp Leu Val Glu Glu Asn Phe Glu Glu Arg Val  
 325 330 335  
 Lys Gly Gln Gly Leu Leu Ile His Gly Trp Ala Pro Gln Val Leu Ile  
 340 345 350  
 Leu Ser His Thr Ser Ile Gly Gly Phe Leu Thr His Cys Gly Trp Asn  
 355 360 365  
 Ser Ser Val Glu Gly Ile Ser Ala Gly Val Pro Met Ile Thr Trp Pro  
 370 375 380  
 Met Phe Ala Glu Gln Phe Cys Asn Glu Arg Leu Ile Val Asn Val Leu  
 385 390 395 400

Lys Thr Gly Val Lys Ala Gly Ile Glu Asn Pro Val Met Phe Gly Glu  
 405 410 415  
 Glu Glu Lys Val Gly Ala Gln Val Ser Lys Asp Asp Ile Lys Met Val  
 420 425 430  
 Ile Glu Arg Val Met Gly Glu Glu Glu Glu Ala Glu Met Arg Arg Lys  
 435 440 445  
 Arg Ala Lys Glu Leu Gly Glu Lys Ala Lys Arg Ala Met Glu Glu Gly  
 450 455 460  
 Gly Ser Ser His Phe Asn Leu Thr Gln Leu Ile Gln Asp Val Thr Glu  
 465 470 475 480  
 Gln Ala Asn Ile Leu Lys Ser Ile  
 485

<210> 9

<211> 1669

<212> DNA

<213> Petunia hybrida

<220>

<223> Nucleotide sequence coding for a protein having  
glycosyl transferase to aurone

<400> 9

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 Met  
 1  
 ggt cag ctc cat ttt ttc ttc ttt ccc atg atg gct cat ggc cac atg 164  
 Gly Gln Leu His Phe Phe Phe Phe Pro Met Met Ala His Gly His Met  
 5 10 15  
 att cct aca cta gac atg gct aag ctt ttc gct tca cgt ggt gtt aag 212  
 Ile Pro Thr Leu Asp Met Ala Lys Leu Phe Ala Ser Arg Gly Val Lys  
 20 25 30  
 gcc acc ata atc act act cct ctc aat gaa tca gtt ttc tcc aaa gct 260  
 Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys Ala  
 35 40 45

att gaa aga aac aag cat gaa att gac atc cgt ttg atc aaa ttc caa 308  
Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe Gln  
50 55 60 65  
gct gtt gaa aat ggc ttg cct gaa ggt tgt gag cgt att gat ctt atc 356  
Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu Ile  
70 75 80  
cct tct gat gac aag ctt tcc aat ttt ttg aaa gct gca gct atg atg 404  
Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Ala Met Met  
85 90 95  
caa gaa cca ctt gag cag ctt att gaa gaa tgt cat ccc aat tgt ctt 452  
Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys Leu  
100 105 110  
gtt tct gat atg ttc ctt cct tgg act act gat act gca gcc aag ttt 500  
Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys Phe  
115 120 125  
aac att cca aga ata gtt ttc cat ggt acg agt ttc ttt gca ctt tgt 548  
Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu Cys  
130 135 140 145  
gta gag aat agt aac agg act aat aag cca ttc aag aac gtc tct tct 596  
Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser Ser  
150 155 160  
gat tct gaa act ttt gtt gta cca aat ttg cct cac gaa atc agg cta 644  
Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg Leu  
165 170 175  
act aga aca caa ttg tct ccg ttt gag caa tca ttg gaa gag aca cca 692  
Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr Pro  
180 185 190  
atg tcc cga atg ata aaa gca gtt agg gaa tcg gac gcg aag agt tat 740  
Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser Tyr  
195 200 205  
gga gtt atc ttc aac agc ttc tat gag ctt gaa tca gat tat gtt gaa 788  
Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val Glu  
210 215 220 225  
cat tat acc aag gtt ctt ggt aga aag tct tgg gct att ggc ccg ctt 836  
His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro Leu  
230 235 240

tct ttg tgc aat agg gac att gaa gat aaa gct gaa aga ggg aag att 884  
 Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys Ile  
 245 250 255  
 tcc tct att gat aaa cat gag tgt ttg aat tgg ctt gat tca aag aaa 932  
 Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys Lys  
 260 265 270  
 cca agt tcc att gtt tat gtt tgc ttc ggg agc gta gca gat ttc act 980  
 Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe Thr  
 275 280 285  
 gca gca caa atg cgt gaa ctt gca ttg gga att gaa gca tct gga caa 1028  
 Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly Gln  
 290 295 300 305  
 gaa ttc att tgg gct gtt aga aga ggc aaa gag gaa caa gac aat gaa 1076  
 Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn Glu  
 310 315 320  
 gag tgg ttg cct gaa gga ttc gag gaa aga acg aaa gaa aaa ggt cta 1124  
 Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly Leu  
 325 330 335  
 att att aga gga tgg gcg ccc caa gtg cta att ctt gat cac caa gct 1172  
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 340 345 350  
 gtg gga gct ttt gtc act cat tgt ggt tgg aat tca acg ctt gaa gga 1220  
 Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly  
 355 360 365  
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 Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu Gln  
 370 375 380 385  
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 Phe Phe Asn Glu Lys Leu Val Thr Glu Val Leu Arg Thr Gly Ala Gly  
 390 395 400  
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 Val Gly Ser Met Gln Trp Lys Arg Ser Ala Ser Glu Gly Val Lys Arg  
 405 410 415  
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 Glu Ala Ile Ala Lys Ala Ile Lys Arg Val Met Val Ser Glu Glu Ala  
 420 425 430

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 Gln Asp Ile Ser Thr Tyr Ser Ser Lys Ser His  
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 Lys Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys  
 35 40 45  
 Ala Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe  
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 Gln Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu  
 65 70 75 80  
 Ile Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Met  
 85 90 95  
 Met Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys  
 100 105 110  
 Leu Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys  
 115 120 125

Phe Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu  
 130 135 140  
 Cys Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser  
 145 150 155 160  
 Ser Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg  
 165 170 175  
 Leu Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr  
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 Pro Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser  
 195 200 205  
 Tyr Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val  
 210 215 220  
 Glu His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro  
 225 230 235 240  
 Leu Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys  
 245 250 255  
 Ile Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys  
 260 265 270  
 Lys Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe  
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 Gln Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn  
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 Glu Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly  
 325 330 335  
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 Gly Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu  
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 385 390 395 400  
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 Arg Glu Ala Ile Ala Lys Ala Ile Lys Arg Val Met Val Ser Glu Glu  
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Ala Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys  
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